4. (Twice Amended) A method for developing lead compounds for an inhibitor of bacterial IMPDH (inosine monophosphate dehydrogenase), said method comprising:

[a.](a) obtaining a crystal of bacterial IMPDH;

[b.](b) recording x-ray diffraction data from said crystal;

[c.](c) using said diffraction data to generate an electron density map consistent with a [the] model for the molecular structure of a binding pocket of IMPDH; and

[d.](d) developing lead compounds for an inhibitor of bacterial IMPDH based on the map of three dimensional structural information of the molecular structure of the binding pocket of IMPDH.

6. (Twice Amended) A crystalline molecule or molecular complex comprising [all or any parts] of a binding pocket wherein said binding pocket is defined by structure coordinates of IMPDH amino acids 50-56, 75-80, 229-235, 252-260, 283-286, 302-322, 343-345, 365-432 and 449-455, according to Table 7, or a homologue of said molecule or molecular complex, wherein said homologue comprises a binding pocket that has an amino acid sequence identity for the corresponding binding pocket residues of 60% or greater relative to the *S. pyogenes* IMPDH binding pocket.

7. (Twice Amended) A crystalline IMPDH molecule defined by structural coordinates for IMPDH amino acids [comprising coordinates] from *S. pyogenes* IMPDH amino acids 50-56, 75-80, 229-235, 252-260, 283-286, 302-322, 343-345, 365-433, and 449-455.

REMARKS

I. Status of the Claims

Applicant thanks Examiner Marschel for allowing claims 3 and 4, and potentially allowing claim 2 with a dependency amendment.

However, applicant requests clarification of the status of some other claims. The Interview Summary form only says claims 1 - 7 were discussed. The Advisory Action lists 1 - 8. Our records show claims 1 - 8 are pending.

We note that the amendments of February 13 and May 6, 2002 were not entered. Applicant had already cancelled claim 5 in the amendment mailed May 6, 2002, but claims 1 - 4 and 6 - 8 were still pending. Applicant now cancels claims 1 and 8 and again cancels claim 5, reserving the right to prosecute them in a continuing application.

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WE CLAIM:

2. The crystal of claim 3 further characterized by ability to provide x-ray diffraction patterns useful to define molecular structures for bacterial IMPDH enzymes.

F1

3. A crystal of bacterial IMPDH (inosine monophosphate dehydrogenase) isolated from a bacterial preparation wherein the bacterial preparation is a pure culture of *Streptococcus pyogenes*.

4. A method for developing lead compounds for an inhibitor of bacterial IMPDH (inosine monophosphate dehydrogenase), said method comprising:

F2

(a) obtaining a crystal of bacterial IMPDH;

(b) recording x-ray diffraction data from said crystal;

(c) using said diffraction data to generate an electron density map consistent with a model for the molecular structure of a binding pocket of IMPDH; and

(d) developing lead compounds for an inhibitor of bacterial IMPDH based on the map of three dimensional structural information of the molecular structure of the binding pocket of IMPDH.

6. A crystalline molecule or molecular complex comprising a binding pocket wherever said binding pocket is defined by structure coordinates of IMPDH amino acids 50-56, 75-80, 229-235, 252-260, 283-286, 302-322, 343-345, 365-432 and 449-455, according to Table 7, or a homologue of said molecule or molecular complex, wherein said homologue comprises a binding pocket that has an amino acid sequence identity for the corresponding binding pocket residues of 60% or greater relative to the *S. pyogenes* IMPDH binding pocket.

F3

7. A crystalline IMPDH molecule defined by structural coordinates for IMPDH amino acids from *S. pyogenes* IMPDH amino acids 50-56, 75-80, 229-235, 252-260, 283-286, 302-322, 343-345, 365-433, and 449-455.